

FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
GTTGAAGGGTGTTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTCTTACACAGTG
TCTGAGAACATTTACATTATAGATAAAGTAGTACATGGTGGATAAATCTTACTTTTAGGAGGA
CTACTCTCTTCTGACAGTCTTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG
CTCCTATTATTCTGTGCTTTGTGCTCTGCCAAACCTTCTTTAGCCCTTCACACATCGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACAGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACCTCTCTTTTTTCCAACAAGAGAGCCAAAGACCATTTTTTCCA
TTTGATCTGTTTTCCAATGTGTCCATTGGATGTCAGTGCTATTACAGAGTGTGTACATTGTCTC
AGATTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTGTGATACTCGAATGCTTGATCTTC
AAAACAATAAAATTAAGGAAATCAAAGAAAAATGATTTTAAAGGACTCACTTCACTTTATGGT
CTGATCCTGAAACAACAAGCTAACGAAGATTACCCAAAAGCCTTTCTAACCACAAAGAA
GTTGCGAAGGCTGTATCTGTCCCAACATCAACTAAGTGAAATACCACTTAATCTTCCCAAT
CATTAGCAGAACTCAGAATTCATGAAAAATAAGTTAAGAAAAATACAAAAGGCACATTCAAA
GGAATGAATGCTTTACACGTTTTGGAAATGAGTGCAAACCTCTTGATAATAATGGGATAGA
GCCAGGGGCATTTGAAGGGGTGACGGTGTTCATATCAGAATTGAGAAGCAAACCTGACCT
CAGTTTCCTAAAGGCTTACCACCACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTCA
ACAGTGGAACCTTGAGGATTTTTAAACGATACAAAGAACTACAAAGCTGGGCCCTAGGAAACAA
CAAAATCACAGATATCGAAAAATGGGAGTCTTGCTAACATACCAGTGTGAGAGAAATACATT
TGGAACCAATAAACTAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
ATCTTCCTTCATTCTAATTCAATTGCAAGAGTGGGAGTAAATGACTCTGTCCAACAGTGCC
AAAGATGAAGAAATCTTTATACAGTGCAATAAGTTTATTCAACAACCCGGTGAAATACTGGG
AAATGCAACCTGCAACATTTTCGTTGTGTTTTGAGCAGAATGAGTGTTCAGCTTGGGAACCTT
GGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT
TGGAATACTTGAACCTCTATTATAATGGTAGTATTATATATACAAGCAAAATATCTATTCTCA
AGTGGTAAGTCCACTGACTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT
CTTACATAAAGGGTTGAGAGCAACAAGCATCTATTGCAGTTTCTTTTTTGCGTACAAAATGAT
CTTACATAAATCTCATGCTTGACCATTCCCTTTCTTCATAACAAAAAGTAAGATATTCGGTA
TTTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAAATGGAATGCTTGACT
TAGCAAAATTTGTGCTCTTTCATTTGTCTGTTAGAAAAACAGAATTAACAAAGACAGTAATGT
GAAGAGTGCAATTACACTATTCTTATCTTTAGTAACTTGGGTAGTACTGTAAATTTTTTAAT
CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCCCGT
CTTTATGTTTTAAACCTAAATTTCTTAAATAAAGCCTTCAGTAAATGTTTCATTACCAACTTGA
TAAATGCTACTATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTAATTATT
ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTTCATAAAATCTGTAACCTCGCATTTT
AATGATCCGCTATTATAAGCTTTTAATAGCATGAAAATGTTAGGCTATATAACATTGCCAC
TTCACTCTAAGGAATATTTTTTGAGATATCCCTTTGGAAGACCTTGCTTGGGAAGAGCCTGGA
CACTAACAAATTTACACCAAAATGTCTCTTCAAATACGTATGGACTGGATAAATCTGAGAAA
CACATCTAGTATAACTGAATTAAGCAGAGCATCAAATTAACAGACAGAAACCGAAAGCTCTA
TATAAATGCTCAGAGTCTTTTATGTATTTCTTATTGGCATTCAACATATGTAAAATCAGAAA
ACAGGGAATTTTCATTAATAAATATTGGTTTGAAAT

0394457.063601

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFPMCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNKLTKIHKPAFLTTKKLRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANIPRVREIHLENNKLKKIPSGLP
KYLQIIFLHSNSIARVGVNDFCPTVPKMKKSLYSAISLFNPNVKYWEMQPATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLLGLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHPDLGQPFQVMRCVLCACEAPQWGRTRGPRGVSCKNIKPECTPTACGQPRQLPGHCCQT
CPQERSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAERARGDGHTDFVALLTGPRSQAVAR
ARVSLRRSSLRFSISYRRLDRPTRIRFSDSNGSVLFHEHPAAPTQDGLVCGVWRAVPRLSRL
LRAEQLHVALVTLTHPSGEVWGPIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGQLLRELQANVSAQEPGFAEVLNPLTVQEMD
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLQSVLCGADALI PVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVVAMTLETKPQRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML
LQNELFLNVGTDKDFDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVVKSAAGHAWLS
LDTHCHLHYEVLLAGLGSEQGTVAHLLGPPGTPGPRRLKGFYGSEAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGRLLEAAGAEVGRALGAPDTASAAPPVV
PGLPALAPAKPGGPGPRDPNTCFEFGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVC
PPSCPHPVQAPDQCPCVCEKQDVRDLPLGLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPFF
GLIKCAVCTCKGGTGVEVHCEKVQCPRLACAQPVVRVNPDTCCQKQCPVGSAGHPQLGDPMQADG
PRGCRFAGQWFPESQSWHPSPVPPGEMSCITCRGAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRRPETRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

[illegible]

GGCGAGCAGCCCTAGCCCTCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACGCGCGCGCGCTCACTGCG
TCTTGCTCTCCGGCTCTCCGCGCTCTCCGGCGCGC**ATG**CAGCCCCCGCGCGCCAGCGCGCGGCTGCGCAGCTGC
TCCGCGCTCTGCGCCCTGCTGCTGTGCTGTGCTGCGGGCGGGCGCCGAGGCAGCTCTCTGGCCACACCGCTGCGCG
CCGCGCCCTTGTCTGCGCCCGGGCGCGCGCGCGCAGCCTGCCGGAAATGGCGGCTGTGTGACACTCTCGCGCCCTT
AGCCGACAGCCGACAGCCAGCGGCCCGCGCGCAGCTGGTCAAGCTGACCTGCGCCCGGGATCTCTCGGCG
CCAACTGCGCAGCTGTGTGCAGATCTTGTGCCAGCAACCTTGTACCATTGGCAACTGACAGCAGCAGCAGCAGCA
GCGACGCGCATGGTCTACCTCTGCATTGCAATGAAGGCTGTGAAGGTTCCAACTGTGAACAGCAGCTCTCCAAGTCT
TCCGACGACTGGCTGAGCAAGTCCATGACCCCGACAGCTCAGCGCTGTCTCGTCTCACTCAGGAGCTGTGACA
AAATCTGCTCCTCGCTCTCAGGCAACGGTGTGACACTCTTACCTCGCAGCGCAGAAAACAGGCGAGAAAGTTGTAGAAA
TGAATGGGATCAAGTGGAGTGTACAGATATGTGCTTGTGGGAATGGCAATTCTAACAGCTCTCGCGGTGGCC
GCTGTGATCTCTTGAAGTGCACAGAACTCTCAGTCAAGATTTCGGCAAGATGCCACTGCTCTCACTGATTTTGC
TCTGGAAGTGCACGGCCAGAGGTTTCAACAGTGTCTCCCTCATAGATGACGAAGATGTGACCCCTCTCAGCGTCT
CAGGGGACTGTGCTCTCTGGAGAGATGTCTGCGCTTGGGAAAATAATCACTATTGGTTTGTGAATGATTTCTG
TGACTAAGTCTATTGTGGTTTGTGCGTCTAACTCTGTGTGGAAGTGCAGCTGCTGTGCCCGGGGAGAGTTCAG
CAATGACTTTGGAGTGTTCAGAAAAGGAAATGACAGTGAAGGCGCTCAGGCGCAACTTTTTCTGTACCTGTG
AGGAGCAGTACGTGGGTGATCTGTGAGAAATACGATGCTTGCAGAGGAAAACCTTGCACAAAACAGCGAGCT
GTATTGTCCAAATGAAGGCAAGATGGGAGCAATTTCACTGTGTTTGGCTTCTGGTTATACATGGAGAGTCTT
GCCAGTCCAAGATTGATTACTGCATCTAGACCATTCAGAAATGAGACAAATGCATTCTCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGATATCTCGGATCTGCTTGTGAGAAGAAAGTGAGCCCTTGGCGCTCTGCTCTCGT
CGCAGAAACAGCGCACTGCTATGTGAGCAGGGGTACACTTTCATCTGCAACTGCAGCGCGGCTCTACAGGCGCA
CTTGTCGCGCAGCTATTGACTCTCTGTCCTCAGCCCTCAGCCCTCTGCTCATGACAGTGGCCGACGCTGGGCGACAGCT
CAAAATGGCTCTGTGATCTCAGTTTACCATTGGCTCTACTGTGGAGGAGGAATAATGAGTGGCTCTCCGCTTCAAT
GCTGAATGCAGCCACCTGCAGGGAACCTGTTAATGGCTATGAGTGTGTGCTCGCAGCAATAACAGAAACAC
ACTGTGAATTTGTACAAGGATCTGCTCCGCTAACGCTCAGCTGTCTGACAGCGACCACTGTGAACAGCGACGCGCTTCA
ATGGCAGCTGCATCTGTGCAACCGGGTTTACAGGTGAGAGTGCACATTTGACATTAATGAATGTGACATGCGA
CTTGCCACCACTGTGTGGAGCGTCTGTGCAGGACCCTCAATGTTTAACTATGCACTGCCACTGCCCGCATGGTTGGGTGGAG
CAAACTGTGAGATCCACTTCAATGGAAGTTCGGGACATGGCGAGAGCTCCACCAACATGCCCGCGCACTCCC
TCTACATCATCATTTGAGAGCCCTCTGCGTGGCTTCTATCCTTATGCTGATCATCTGATGTGGGGATTTGGCGCA
TCAAGCCGCAATGGAATACAGGCTTCTTCCAGCGCAGCTCTATGAGGATTTCTACAACTGCGCGCAGCATCGACAGCG
AGTTTCAAGAAATGCCATTCTCATCTCCGAGTGCAGGTTTGTGAAGAATAACCCGGCTGCAATGTATGATGTGA
GCGCCATCGCCTATGAAGATATCAGCTGCTGATGACAAACCTGGTCACTGATTAACAACTAAAGATTTG**TAAT**
CTTTTGTGGATTAATTTTCAAAAAGATGAGATACATCACTAATTTAAATATTTTAAAGAAAATAAAAGCTTAA
GAAATTTAAATGCTAGCTGCTCAAGAGTTTTCAGTAGAATATTTAAGAACTAAATTTTCTGCAGCTTTTAGTTTG
GAAAAAATATTTAAAAACAAAATTTGTAAACCTATAGACAGTTTAAATGATCTCAGCTCTCTAAAGCTT
GTGCTTCTACTAGTGTGTGCTTTTCTCACTGTAGACATATCAAGACGCAAGCAATAATTTCTGTGGTTGTACA
GAATAGCTCTAATCAGGAGAGTTTCTGTTGACGTTTGAAGTGGCGGCTTCTGAGTAGAGTTAGGAAAATCCAC
GTAAGCTAGCATATGATATGATATAAGATACACCGTATCTAAAGAAAGTCTGAATATGCTGTTTGTGGAAA
AGAAACTAGTATAATTTACTATTTCTTAACCGGAATGAAATTAGCCTTTGGCTTATTCTCTGTGCATGGGTAAAGTAACT
TATTTCTGCACTGTTTGTGAACTTTGTGGAACCTTTGTGAGTTTGTGTTTGTGATCTTGTGAACAGATTT
TCGAACTAGGCCCTCAAAAACATAGTAACGAAAGGCTTAGCGAGCAAAATCTGATTGATTGAACTATATTT
TCTTTTAAAGAGCTCAGGGTCTTATATTTGTAGTAATAATTAATTTACATTTGAGTGGTTTGTGCTCAGAGGATG
TAAATGTAAAGAGAGTACGGTCTCTCAGTAGTGAGTATTTCTCATAGTGCAGCTTTATTTATCTCAGAGATGTT
TTGTGGCTGTATTTGATTGATATGTGCTTCTCTGATTCTCTGTAATTTCCAACCAATTGAAATAAATGTGATC
AAGTCA

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDPQHPAPAGEPGYSCTCPAGISGANCOLVADPCASNPCHHGNCSSSSSSSSDGYLCICN
EGYEGPNC EQALPSLPATGWTESMAPRQLQVPATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVFPQNTSVKIRQDATASLILLWKVTATGQV
QCSLIDGRSVTPLQASGGLVLLEEMLALGNNHFIGFVND SVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSCTCEEQYVGTFCEEYDACQKRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYICILDPCRNGATCISLSGFTCQCEGYFGSACEEKVDPC
ASSPCQNNGT CYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSTYKCLCDPG
YHGLYCEEYNECLSAAPCLNAATCRDLVNGYECVCLAEYKGT HCELYKDP CANVSCNLNGATC
DSDGLNGTCICAPGFTGEECDIDINECDSNPCHHGSCLDQPNGYNCHCPHGWWGANCEIHL
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISR IEYQGSSRPAYEEFYN
CRSIDSEFSNATASIRHARFGKSRPAMYDVSP IAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTTCAGGCTTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTTATTGGTTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAAC
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTCC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTCACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAAGTGAATGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

100
90
80
70
60
50
40
30
20
10
0
100
90
80
70
60
50
40
30
20
10
0

FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTTCAGGCTTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAAC
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTCACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAAGTGAATGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

6394457.063001

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCCAGCCTGTAACCTGTGCCCTACACCAGCCAG
GCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCACACCATGCCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCTTGGTCCTAAGGCAGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCTTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGA
AAGTGGTGGCAGAAATGAACCGCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC
GGGTGTGTGCAACAGTGTCTCGGAATGTTCTCTGATGACATCCTGCAGCTTCTGAAGAAGA
GGTGGCGTCTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGC AACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCTATGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGTCTCTGATAGAGGAGTTGCTGAGTCTGGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCC
TCGTGGAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCTTGGAGGACAAGTTCCTCGGATGAGCAGCTGAGCAGTTCTCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACCTACTGAGATTCCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCTCCCCCACATGGCCCCAG
TCCTTGCAAGTTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCCTGTTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTTGGACATAG

CGGAGGCTGCTGCTGCTGCTGCTGCCAGCCTGTAACCTGTGCCCTACACCAGCCAG

[illegible]

THE UNIVERSITY OF CHICAGO

[illegible]

THE UNIVERSITY OF CHICAGO

[illegible]

THE UNIVERSITY OF CHICAGO

[illegible][illegible][illegible]

THE UNIVERSITY OF CHICAGO

THE UNIVERSITY OF CHICAGO

06707

AAAACCTATAAATATTCGGGATTATTCATACCGTCCCACCATCGGGCGGGATCCGCGGCCG
 CGAATTCTAAACCAACATGCGGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCAGCA
 CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC
 AACGACCTGCCCTTGGTCCTAAGGCGAGGTTACAGAAAGGGCTACAGGATGTAACTCGCG
 CAATTTGAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCAGT
 TCTGGTGAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTTGAG
 CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
 TAAAGCTCTGAACGACACTCAGAAATTTGGCCTGCCTCATCGTGTAGAGGGTGGCCACTGCT
 TAGGACAATAGCTCTCCATCTTACGTACCTTCTACATCTGAGGAGTCCGCTACTCTGACCTCA
 ACCCAACATGCAACACACCTTGGGACAGAGACTCCGCTTAAGGCGTGCATCCTTCTACAA
 CAACATCAGCGGGCTGACTGACTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCTTGGCA
 TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCTGGAAGTGTACAG
 GCACCTGTGATCTTCTCCCACCTCGGCTGCCCGGGGTGTGTGCAACAGTGCTCGGAATGTTC
 TGATGACATCTTCGAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG
 GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
 AAGGCTGTCAATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
 CCTTCAGGGGCTGGAAGACGTGTCCACATACCCGCTCTGATAGAGAGATTGCTGAGTCGTG
 GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAACCTGCTGCGGGTCTTCAGACAA
 GTGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCTTGAGGAGACAAGTTCGCGATGA
 GCAGCTGAGCAATTCTGCCACTCCGACCTCTCAGTCTGCGTCAGAGACAGAGTCTGACTT
 CAGGCCAGGAAGTCTCAGTAGATCCCATACACTGGAACAGCCAAAGTTACGAGCAAGTGGTCA
 GTCTCAGAGTCTCCCTCCACCTTGACAAAACTACACATCCGCTCCGTCAGCCAGCACTGA
 ACTCTGGGGGGACGCTCAGTCTTCTCTTCCCCCAAAACCCAAGGACAC

00000000000000000000000000000000

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX (S/T): 5
MPGTYPAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRLDGLVGAQFWASAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPNSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYFVLIEELLSSRGWSEBELQGVLRGNLLRVFRQVEKQVEENKWQSPLEDKFPDEQLSSS
CHSDLRLRQRQKSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDPDKTHTCCPAPPELLGGP
SVFLFPKPKDPT
```

FIGURE 13

CGCCAGCGACGTGCGGGCGGCCTGGCCCGCGCCCTCCCGCGCCCGGCCCTGCGTCCCGCGCC
 CTGCGCCACCGCGCCCGAGCCGAGCCCGCGCGCCCGCGGCAGCGCGGCCCCATGCCC
 GCCGGCCGCGGGGGCCCCCGCCCAATCCGCGCGGGCGGCCCGCGCGTGTGCGCCCTGCT
 GCTGTGCTCTGCGTCTCGGGGCGCCGAGCCGGATCAGGAGCCACACAGCTGTGATCA
 GTCCCCAGGATCCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGACCGGA
 GACCCACAGGAGCCACCGCGGAGGGCCTCTACTGGACCCCTCAACGGGCGCCGCTGCCCCC
 TGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAACTCAATGGGT
 CCAGGCAGCGGTGCGGGGACAACCTCGTGTGCCACGCCCGTGACGGCAGCATCCTGGCTGGC
 TCCTGCCCTCTATGTTGGCTGCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA
 CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACGGGGAGACCTTCTCCACACCA
 ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC
 ACAGTGGGGCCCCACTCCTGCCACATCCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT
 CTGGGTGGAGGCCACCAACCGCTGGGCTCTGCCCGTCCGATGTACTCACGCTGGATATCC
 TGGATGTGGTGACCACGGACCCCCGCCCGACGTGCACTGAGCCGCGTGGGGGCTGGAG
 GACCAGCTGAGCGTGCGCTGGGTGTGCCACCCGCCCTCAAGGATTTCTCTTTCAAGCCAA
 ATACCAGATCCGTACCGAGTGGAGGACAGTGTGGACTGGAAGGTGGTGGACGATGTGAGCA
 ACCAGACCTCCTGCCGCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCTGTCAAGTGGC
 TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGTGGAGCCACC
 CACAGCCGCTCCACTCCCAGTGAGCGCCCGGGCCCGGGCGCGGGCGTGCGAACCGC
 GGGGCGGAGAGCCGAGCTCGGGGCGGTGCGGCGCGAGCTCAAGCAGTTCTGGGCTGGCTC
 AAGAAGCACCGCTACTGTCTCAACCTCAGCTTCCGCTCTACGACCAGTGGCGAGCCTGGAT
 GCAGAAGTCGACAAGACCCGCAACCAGGACGAGGGGATCCTGCCCTCGGGCAGACGGGGCA
 CGGCGAGAGGTCTTGCAGATTAAGCTGTAGGGGCTCAGGCCACCTCCTGCCACGTGGAGA
 CGCAGAGGCCGAACCCAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACCTGAGCCAC
 CCTCAGCAGGAGTGGGTGGCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCACGT
 GAGGCCACCTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC
 CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC
 CCTCCAAAGAGTCCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATTGTGAAAAA
 AA

CGCCAGCGACGTGCGGGCGGCCTGGCCCGCGCCCTCCCGCGCCCGGCCCTGCGTCCCGCGCC

FIGURE 15

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
 AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
 CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCTTCGTTGAAGCTTTTTATTCTCTAA
 GAGGAGAAAAATCAGTACC GGCGAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA
 GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCCTCTGGGATATAAATAAG
 CATGGAAGTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCTACCTTTGT
 GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGTCTACA
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
 GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCAGTGTGGCTTCGGCAG
 CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGTCTTGGGA
 TTTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
 TCTGTGTCCTAATTTTCGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTTGGGACCCA
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
 ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAGGATCCTTCCTGAGCGTTT
 CCTGGCAGTTTTAAAAACGAAAAATCAGTGTAAAGTTTGATGCAGTTATTGGATATAAAATGA
 AAGCGCAATAAGCACCTAGTPTTCTGAAAACGATTTACCAGGTTTAGGTTGATGTCTATCA
 ATAGTGCCAGAAATTTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTCTTCAATA
 TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCCTTGTCTTTAGCCAAAAGCTGATT
 ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAATGAAGAAAAAGAA
 CCAAAATGACTTTATTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
 AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTGTATTGCACTTAAATTTTGT
 ATAATTTGTGTTTTCTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
 TGAAGGACTATATCTAGTGGTATTTTACAATGAATATCATGAACCTCTCAATGGGTAGGTTTC
 ATCCTACCATTGGCACTCTGTTTTCCTGAGAGATACCTCACATTTCCAATGCCAAACATTTCT
 GCACAGGGAAGCTAGAGGTGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
 GAGAATTGAGAGAATGTACCCACAAATGCGAGCAATAATAAATGGATCACACTTAAAAAAA
 AA
 AA

0394457.05301

FIGURE 16

```
</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436
<subunit 1 of 1, 300 aa, 1 stop
<MW: 32964, pI: 9.52, NX(S/T): 1
MKFLLDILLLLPLLVCSLESFVKLPIPKRRKSVTGEIVLITGAGHGIGRLTAYEPAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKQA
```

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

00000000

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCCAGGAGCCGGCAGGAGCAACCAAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCTTGGCCGGGGAGAAAGCGCGGGGGCTGGAGCACCAACCA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
GCGAGAGGACCCCGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC
TGCTCCTGGGCCTTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCAGCCTCTGC
CCGGGGCACCCCGGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCG
CGATGGCCCGCAGCGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG
CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCTTGCCCTTCGACCCGCTGTGTTGAACG
AGCAGGGACATTACGACGCCGTACCGGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
ATCCATTGCTCTTTCTTCCAGTTTTTTCGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGG
GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGATTCTTGGTGTACTCCGA
CTGGCACAGCTCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCTATCCAGGAGGCTGGCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTCTGTCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCACGGT
GGGGTGCTCTCTTCTGGTCTCTGCTTCTCTGGATCCTCCCCACCCCTCTGTCTCTGGG
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCTCATAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP
GEKGEGRPGPLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFEAKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLPEPDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

[illegible]

CTCTTTTGTCCACAGCCAGCCAGCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCTTGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCTTGCAACAACCGCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCCAATGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG
CAAGTGGGCTGGAAATGCAGCTGCTGCCCGGGCTTGGCGTCTTTGTTGAAGTGGTCAG
CCTATGGTTTGACAGAGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTGTCTGTGCCTACTCCCCCGAGGCCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCTTATAAGAAGGGTGCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAGGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGACGCTGCAGCTGCAGTGTGTGC
ACGGCCGGTTCGGGAGGAGGAGTGTCTCGTGCCTCTGTGACATCGGCTACGGGGGAGCCCA
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTGAGAGGAAAGGCG
GGGTGTGTGGCCAGATCAAGAGCCAGAAAGTGACAGGACATCCTCGCCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTTCGAGACCAGGAACTTCTGGATCGGGCT
CACCTACAAGACCGCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAGGCCTTACCA
GTTTTGCCTTTGGGCAGCCTGACAACACGGGCTGGTGTGGCTGAGTGTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTC
GAGGCCTGACCACATGGCTCCCTCGCCTGCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAGAGGTCTCAGA
CCTTGCACAATGCCAGAAGTTGGGCAGAGAGAGGAGGAGGAGGAGGAGTGGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGCGCAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTCCACCTGGCCAGAG
CCTGTGGGGCAGCGAGCTTCCCTGTGGCATGAACCCACGGGTATTAATATGAATCAG
CTGAAAAAAAAAAAAA

FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176
<subunit 1 of 1, 455 aa, 1 stop
<MW: 50478, pI: 8.44, NX(S/T): 2
MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWV
QPPAADMRRLDWSLSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRNLNSTCH
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAGCATKVHFFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTETNEVTDSDFETRNFwig
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGPGS
```

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCCGAGCGTCCCGCGCCCT
CGCCCCCGCCATGCTCCTGCTGCTGCGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTGC
GGAAGAGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG
TCAGACTGTTGCAGAGGCTGAAAAACCAACCTTTGATGACAGAATTCAGTGAAGTCTACC
ATCATTTCCCGTTATGCCTTCACTACGGTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTTCATCACCACCTTCAGTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAAGAGTGGTGATAGG
GTAAAAAGAGAAAAGGAATAAAACACAGAAGAAAAATGGAGAGAAGGGGACTGAAATATTAG
AGCTTCTGCAGTGATTCCACAGCAAGGACAAAGCCGCTTTTTCCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCAACAACAGCAGGCAGAGGGGCGAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCCAT
CTACTGTCAATTAACAAAATGAACATTGTGCCAACATAATTTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTC AATAG
AGAACAGAGCATTTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCTCA
AAGACCTTCTCCTTTACCCAAGAATGTGGTATTCTGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACCTCCGGCAGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGATCATCACCATATGTCACCCACTGGA
GGCAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA
CAGTGGCATTTGGAGACCGGGAGCGTGTCCCTCATCGTCTTCTGACGGATGGGAAGCCACGG
TCGGGGAGACGCACACCTCAAGATCCTCAACAACACCCGAGAGGCCGCCGAGGCCAAGTC
TGCACTCTTCAACATTGGCATCGGCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTGCT
GGAGAACTGTGGCTTCAACGGCGCGTGCACGAGGAGGAGACGAGGCTCGAGGCTCATCG
GGTTCACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCTGTTCCCAACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGACAGGAAGCTGGATCACCTGCACGTGGAGGTCAACGCCAGCAACA
GTAAGAAATTCATCATCCTGAAGACAGATGTGCTCTGTGCGGCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCTTGGAGGCGATGGAGAGGGGGACCAACCATCGAGCGTCT
CTGGAGCTACCTCACCACAAAGGAGCTGCTGAGCTCCTGGCTGCAAAAGTGACGATGAACCGG
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCATCTCC
TTCACCTCATGAAGCTGAGGGGGCCGCTCCACGCGATGGATGGCTGGAGGAGGCCCAAGC
CATGTGCGGCTGCCATGGGACCCGAACCGGTGGTGACAGCGTGCAGGAGCTGGCACGCAGC
CAGGACCTTTGCTCAAGAAGCCAAACTCGTCAAAAAAACAACCAACCAACCAACCAACCA
CATGGGAGAGATGGTGTTTTTCTCTCCACCACCTGGGGATACGATGAGAGAAGATGGCCACCT
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGTGCGACCTGATCTTGGACCTC
CCAGCTCAGAACTGTGAGAAATAAATGTGTTTTTAAGCTAAAAA AAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

03941457.03909

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLRKLTKPLMTEFSVKSTIIIS
RYAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS
VDVNILESAGIASLEVLP LHN SRQ RGS GRG EDDSG PPPSTVINQNETFANIIFKPTVVQQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTK
LRQTKDALFTILHDLRPQDRFSIIGFSNRKIKVWKDHLISVTPDSIRDGVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAAARGQVCIF
TIGIGNDVDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEII IAGKLVD RKL D LHLHVEVTASNSKKFII LKTDVPVRPQKAGDVTG
SPRPGDGEGD TNHIERLWSYLT T KELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPTTS
MKLRGPVPRMDGLEEAHGMSAAMGPEFVVQSVRGAGTQPGPLKKPNSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGCGGCGGCGGCTCCCGGGCTCCGGCTTCTGCTGTGCTCTTCTCCGCCGCGG
CACTGATCCCCACAGGTGATGGGCAGAACTCTGTTTACGAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTACGCTACTGAA
TCCCAACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACCTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG
AGCACCTTGGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGACACATTGATGACTTATCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
GTAAACATGTGAAGCCATCGGGAAGCCCAGCCTGTGATGGTAACCTGGGTGAGAGTCGATG
ATGAAATGCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCCTCCCAACAACACCACCACCA
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATCATTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTGTTCAT
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG

0344457 033001

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSIISDEGRYFCQL
YTDPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
KSEVEEWSDMYTVTSQLMLKVHKEDDGVVICQVEHPAVTGNLQTRYLEVQYKQPQVHIQMT
YPLQGLTREGDALELTCEAIGKPPQVMVTWVRVDEMPQHAVLSGPNLFINNLNKTNDNGTYR
CEASNIVGKAHSDMYLVYDPPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYPFHEAKGADDAADATAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGA
CCCGCCAGGAAAGACTGAGGCGCGGGCTGCCCGCCCGGCTCCCTGCGCCGCGCGCCGCTC
CCGGACAGAAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGTCTCTGCTACTGGGCCCT
GGGGCCTGGGGTGCGAGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT
GCACTGCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCTCGCGGGCTGCA
GCTCTTGACCTGTGCAGAACAGATCGCCAGCTTCGCGCTGCCCGGCTGCTGCTGCTGG
ACCTCAGCCACAACAGCCTCTGCGCTCGGAGCCCGCATCTGGACACTGCCAACGTGGAG
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGCG
CAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCTCCGGGGCTGACGCGCTCGCGCTGGCCGGCAACACCCGCATTGCCAGCTGCGGCC
GAGGACCTTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTCGAGGC
CCTGCTTGGCAGCTCTCGGGCTCTTCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACC
CCTTCAACTGCGTGTGCCCTGAGCTGGTTTGGCCCTGGGTGCGGAGAGCCACGTCA
CTGGCCAGCCCTGAGGAGACGCGTGCCACTTCCCGCCAGAACCGCTGGCCGGCTGCTCT
GGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCAACACCAAGTGCACCA
CGAGGCCGTGGTGCGGGAGCCACAGCCTTGTCTTCTAGCTTGCTCCTACCTGGCTTAGC
CCCACAGCGCGGCCACTGAGGCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC
TGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCATGCCACCTGG
GGACACGGCACCACTGGCGTGTGTGTGCCCGAAGGCTTACGGGCCGTGTACTGTGAGAG
CAGATGGGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCAGGCCACACGCTCCCT
GACCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
AAGCGGCTGGTGACGCTGCGACTGCCTCGCTCGCTGAGTACAGGTCACCCAGCTGCG
GCCAACGCCACTTACTCCGTCTGTGTATGCCTTTGGGGCCGGGGCGGGTGCCGGAGGGG
AGGAGGCTCGGGGAGGCCATACCCCCAGCCGTCACCTCAACACAGCCCCAGTCACC
CAGGCCCGCAGGGCAACCTGCCCTCCTCATTGCGCCGCTTGGCCGCGTGTCTCTGGC
CGCGCTGGCTGCGGTGGGGGACGCTTACTGTGTGCGCGGGGGCGGGCTATGGCAGACGGC
CTCAGGACAAAGGCGAGGTGGGGCAGGGCTGGGCCCTTGGAACTGGAAGGTGAAGGTC
CCTTTGGAGCCAGGCCGGAAGGCAACAGAGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
GTGTGAGGTGCCACTCATGGCTTCCAGGGCTTGGCCTCCAGTCACCCCTCCACGAAAGC
CCTACATCTAAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC
GAGCCCTCTGCTGCCACACACGTAAGTTCTCAGTCCCAACTCGGGGATGTGTGCAGA
CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCGAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGAGTCCCTGGGCACGGGGCCCTGCCATGTGCTGGTAAC
GCATGCTGGGCCCTGTGTGGGCTCTCCACTCCAGGCGGACCTGGGGGCCAGTGAAGGAAG
CTCCCGAAAGAGCAGAGGGAGAGCGGTTAGGCGGCTGTGTGACTCTAGTCTTGCCCCAGG
AAGCGAAGGAACAAAAGAACTGGAAGGAAGATGCTTTAGGAACATGTTTCTTTTAA
AATATATATATATTATAAGAGATCCTTTCCATTATTCTGGGAAGATGTTTTTCAAATC
AGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATATGAAGGCCCTTTTGTAAAGAAAA
ATAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVFEN
GITMLDASSFAGLPGLQLLDLSQNIASLRLPRLLLLDLSHNSLLALEPGILDANVEALRL
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNNLSLQALPGDLSGLFPRRLRLAAARNPFNCVCPLSWFGFPWVRESHVTLASP
EETRCHFPFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP
ATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGRHHLACLCPGFTGLYCESQMGQ
GTRPSPTPVTPRPPRLTLGIEPVSPSTSLRVGLQRYLQGSVQLRSLRLTYRNLSPGDKRLV
TLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAGAAAYCVRGRAMAAAAQDKQVGFPGAGFLELEGVKVPLEP
GPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAACTTCTTCCCTTCTGCACCACTGCCGTACCTTTACCCGCCCCGCCACC
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGGTCCCCAGCTC**ATG**CCAGCCTC
ATCTCCTTTCTTGCTAGCCCCCAAGGGCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCCCTCCAGAATGGGAAGGGTATCCCTGGCAGAGTCTCCCGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGAGAGATCCCGGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCTTGCACCTGGTTCCTATTAAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCCGGACCGGGCCTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTCAATAATCCCCGG
GCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCTGGGGTTTGTGAAACTG**TGA**TT
GTGTTATAAAAAGTGGCTCCAGCTTGGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTC
CCCGTTCCTCACTTTTCCCTTTTCATTCCCACCCCTAGACTTTGATTTTACGGATATCTTG
CTTCTGTTCCTCATGGAGCTCCG

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFLAPKGGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLPIN
ATSKDDSDVTEVMWQPALRRRGLQAQGYGVRIQDAGVYLLYSQVLFQDVFTFMGQVVSREG
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KLNLSPHGTF LGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

[illegible]

CACTTCTTCCCTCTCTTCTCTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTCGCGAGAGAC
CTCGGAGACCGCGCGCGGGAGAGCGAGGTCGTCTGGGTGGGGGGGACCTGTGGCTGCTCGTA
CCCGCCCCACCTCTCTTCTGTCAGCTGCGCTCTCTCGGAAGCACTTTTCCCTGCTGTGT
TCCTTACCGAGTCTGTGCATCGCCCCGAGCTTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGCGGCGCGGGAGGAGCGCGCGCGGAGCGAGGCGCCGCGAGGAAGATCGGGC
TCCGTGAGCAGGAGCTCTTGTGGCTGGCTAGCTGCTGCTCTTGCCTTTGCTCTGGT
CCTGATGTCGTGTGCCCATGTTCAGGGGGAGAACAGGAGTGGAGGGGAGTGAAGGAGTGC
CGTCGCTCCGGACCATGCCGAGAGGGCTGAAGAACAAATGAAAAATACAGGCCACGTACG
GACGAGGGGCTCCCTGCTTCCCGGTGCTTTCGCTGTGAAGACCCGGTACCTCCATGTACCC
GGCAGCCGCGGTGCCCGAGATCAACATCACTATTGTAAGGCGAGAGGTTGACCGCGGAG
ATCGAGGCTCCAAGGAAATATGGCAAAACAGGCTCAGCAGGGCGCAGGGGGCACCATTGGA
CCCAAGGGGACAGGGGCTCCATGGGGGCTCTGGGGAGCGGTGCAAGAGCCACTACGCCG
CTTTTCGGTGGGCGGAAGAAGCCATGCACAGCAACCTACTACAGACGCTGATCTTTCG
ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTTACCGGCAAGTCTACTGCTAC
GTGCCGGGCTCTACTTCTTCACTCAAGCTGCACACTTGGGAACAGGAGACCTACTCT
GCACATCATGAAGAACGAGGAGGAGTGTGATCTTTCGCGCAGGTGGGCGACCGCAGCA
TCATGCAAAAGCCAGAGCTGATGCTGGAGCTGCGAGAGCAGGACAGGTGTGGGTACGCCCT
TACAAGGGCGAAGCTGAGAACGCCATCTTTCAGCGAGGAGCTGGAACACCTACCTACCTTCAG
TGGCTACCTGGTCAAGCAGCCACCGAGCCCTTAGCTGGCCGGCCACTCTTCTCTCGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGGCTCTTCCCGATCCCTGAGCTCCGACTC
CCTGGCTTTGGCATTCACTGAGACGCCCTGCACACAGAAAGCCAAAGCATCGGTGCTCC
CAGATCCCGCAGCTCTGGAGAGAGCTGACGCGAGATGAATAACAGGGCGGGCACCCG
GAGAACCTCTGGGACCTTCGCGCGGCTTCTGCGACACATCTCAAGTGACCCGCGAGCG
GAGACGCGGGTGGCGGCGAGGCGCTCCAGGGTGGCGCACCGCGCTCCAGTCTTGTGAATA
ATTAGGCAAAATCTAAAGGCTCTCAAAGGAGCAAGTAAGAACCGTGGAGCAAGAAAGAG
TTGTTATTTTTGTCTTTCCAGCAGCTGTGGCTTCCAAAGGAGAGGCTTTTCAAGTTAG
ACTCTGCTTAAAGAAAGATCCAAAGTTAAAGCTCTGGGGTCAAGGGAGGGGCGGGGCGAG
AAACTACCTCTGGCTTAATCTTTTAAAGCAGCTAGGAAGTCTTTCTGAGGATAGGTGGAC
CTGACATCCCTGTGGCTTTGCGCAAGGCTCTTGTGATCTTCTGAGTCAGAGTCGAGGT
GATGGGGCTGGGGGCCAGGCTCAGCCTCCAGAGAGGAGCTGAGCCCCCTGCCTTGGC
TCCAGGTTGGTAGAAGCAGCGGAAGGCTCTGACAGGTGGCCAGGAGCCCTGGGTCCCCA
GGCTGACAGATTTCTTAGTGGGGGACAGCTCTTGTATCATCTCATGTGTGCTGTGCTC
ACCCCTGTGCCACCTCAGAGCCCTGGGGGTGTGCTCATGCTGCCACCTGACCGCTCGGCT
TTCTGTGCCGCTCCCAACAATCAGCCCCAGAGGCGCCGGGGCTTGGCTCTGTGTTTT
TATAAAGCACTCAAGCAGCATGCACTCTCCATCTCTCTGTTGGTCAAGCATCAGGCT
CCAGCTGTGTGTGTGTGTGGCAGCAAGGCTGATCAGACCCCTTGGCCCCACTGCGCT
CATCCAGGCTCTGACCAGTAGCCTGAGAGGGGCTTTTCTAGGCTCAGAGCAGGGGAGAG
CTGGAAGGGGCTGAAAGGCTCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCTG
AGACAGAGTCAAGAGGAAGTACAGCTCCCAATCACCCTGTGAGGATCAGCTCAGAGG
TGGGTGGCAGGAGGCAATAGCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGGC
GTGTCTCCACGGTGTCTCGCCCTGCCATGGCCACCCAGCATCTGATCTCCAGGAACCC
ATAGCCCTCTCCACCTACCCCATGTTGATGCCAGGGTCACTTGTGTAACCGCTGGGCG
CCCAACCCCGCTGCTCTCTTCTCTTCCCCCCTCCCCACCTGGTTTTGACTAATCTGCT
TTCCCTCTCTGGGCTGGCTGGCGGATCTGGGGTCCCTAAGTCCCTCTTTTAAAGAACT
CTGCGGGTCAAGCTCTGAAGCGGATGTGCTGTGGGCTGCCGGAAGCAGAGCGCACACT
GCTGCTTAAGCTCCCCAGCTTTTCAGAAACATTAAACTCAGAAATTGTTTTCAA

FIGURE 30

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDGRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKIFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP
```

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GCGGAGCATCCGCTGCGGTCTCTGCCGAGACCCCCGCGGGATTCGCCGCTCTTCCC GCG
 GCGCGACAGAGCTGTCTCGCAGCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGTCAGCCTTCTTAAAGCAAATTAAGACCAAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTCTCGGGGAGAAAGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTTGACACTAAGGCTGTCTGCTAGTCAGAAAT
 GCCTCAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTTAAGGGAATC
 AGAGGCAATGAGCCGCTATATACTTCAACTCAAGAAGACTGCATTAATCTTCTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGGACTTACCCAGGAAGATTCTCTTACATGGCCAATTTTACAAGCAGTCACTCCCC
 TAGCCCATCATCACAGATTATTCAAAGCCCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCTCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTTACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCTGAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACACCTCGGCTACTCCAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCGAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTTCTC
 AGCCTCCACGACCCCTCATTTCTACAGTTTTTACACGGGCTGCGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTAATCACTCCGACGGAACGTTACTCAAGACTGGAT
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGACGGAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
 TAGTAACCAAGACCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCTTCTGCTTCCCTTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGCTCTC
 CTGGGTTCAAGCGATTCTCCTGCCTCAGCCTCTTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACTAGGCTGATTTTGTATTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG
 GTCTCAAACCTCCTGACCTAGTGATCCACCTCCTCGGCTCCCAAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTCTGTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG
 GGAACCAAATTAGGTAATTTTGGGTAATCTGCTCTCAAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAAATTTCAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTTCTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTATATGGATTCTCTTAAACCTTATT
 CCAGATGTAGTTCCTTCCAATTAATATTGAATAAATCTTTGTACTCAA

FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVII CFLTRLRSASQNCLKKSLVDVVIDIQSSLSKGIRGNFPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQFSSDQEI AHLLENV SALPATVAVASPHHTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTLTNGVNYPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWLIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

099437 0300

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCCTGTCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAACATTGTCATTGTCAACTATGTAACCTGGGA
ATGTGACAGCAACACAGTGTTTTGATATGTATGAAGCGGATAACTCTGGACCGATGACAAAG
TTTATTACAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTACAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACCTCTGATGCTAAGAAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAGAAACGAAGCTGAACACTGCAAGGCTCTGAGTAAAT
GTGTTCTGTATAAACAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCAACA
GCCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTTGTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATATACAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAAATGAATGGAAATCTTAAAAA

0974560-083007

0974560-083007

0974560-083007

0974560-083007

0974560-083007

0974560-083007

0974560-083007

0974560-083007

0974560-083007

0974560-083007

0974560-083007

0974560-083007

0974560-083007